

REMARKS

Claims 39-62 were pending the application. Claims 43, 44, and 62 have been canceled, without prejudice, and claims 39-53 have been amended. Accordingly, upon entry of this amendment, claims 39, 40-42, and 45-61 will be pending. For the Examiner's convenience, the pending claims are set forth in Appendix A.

Support for the amendments to the claims may be found throughout the specification, including the originally filed claims. In particular, support for the amendment to claim 49 may be found in the specification at, for example, page 23, lines 26-27.

No new matter has been added. Any amendments to and/or cancellation of the claims should in no way be construed as an acquiescence to any of the Examiner's rejections and was done solely to more particularly point out and distinctly claim the subject matter of Applicants' invention in order to expedite the prosecution of the application. Applicants reserve the right to pursue the claims as originally filed in this or a separate application(s).

Objections to the Specification

The Examiner has objected to the specification because "it contains an embedded hyperlink and/or other form of browser-executable code. See page 54."

Applicants respectfully submit that the specification has been amended to delete the embedded hyperlink. Accordingly, Applicants respectfully request reconsideration and withdrawal of the foregoing objection to the specification.

Furthermore, the Examiner is of the opinion that "Appendices A and B do not comply with the sequence rules, specifically 37 CFR 1.821 (d)." The Examiner has objected to the specification "for not being in compliance with the sequence rules." In particular, the Examiner is of the opinion that "[a]s the claims recite SEQ ID NO's, and for purposes of compact prosecution and pendancy reduction, an office action on the merits of the claims follows. However, applicant is advised that all sequence rules must be complied with at

the time of filing of any reply to this office action in order for that reply to be considered responsive.”

Applicants respectfully submit that the instant application is in compliance with the sequence rules, including 37 CFR 1.821(d). Applicants respectfully submit that Appendices A and B contain nucleotide and amino acid sequences which correspond exactly with sequences contained within the Sequence Listing. Each and every sequence listed in Appendices A and B is annotated by a specific Identification Code (e.g., RXN01638, which corresponds to SEQ ID NO:1 and SEQ ID NO:2). For each sequence, the reference number is contained within the Sequence Listing itself. Furthermore, Table 1, which is contained within Applicants' specification, lists each SEQ ID NO and also lists the corresponding Identification Code. Therefore, each sequence contained within the Appendices is readily identifiable with its corresponding SEQ ID NO. Accordingly, Applicants respectfully submit that the instant application complies with the requirements of 37 C.F.R. §1.821(d) and request that the Examiner withdraw the instant objection to the specification.

Rejection of Claims 39, 43-45, 47, and 49-61 Under 35 U.S.C. 112, First Paragraph

The Examiner has rejected claims 39, 43-45, 47, and 49-61 under 35 U.S.C. 112, first paragraph, as “containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.” In particular, the Examiner is of the opinion that

[t]he specification discloses SEQ ID NO: 1. Sequences consisting of SEQ ID NO: 1 meet the written description provisions of 35 USC 112, first paragraph. However, claims 39, 45, 47, 49, and 54-55 recite open claim language (comprising) and are therefore directed to encompass gene sequences, sequences that hybridize to SEQ ID NO: 1, corresponding sequences from other species, mutated sequences, and sequences that have a recited degree of identity (similarity, homology), and so forth. None of these sequences meet the written description provision of 35 USC 112, first paragraph. The specification provides insufficient written description to support the genus encompassed by the claim. It is noted that claims 45 and 47

specifically recite homology limitations, and claim 49 is drawn to a fragment of a nucleic acid. A nucleotide sequence which is 50% different from SEQ ID NO: 1 is a different structure than SEQ ID NO: 1, and would be expected to have different properties (e.g. may encode a different protein or may not encode a peptide at all). The specification does not describe sequences or structures which are 50% different from SEQ ID NO: 1 nor does it disclose any properties of compounds which are 50% different from SEQ ID NO: 1, which would allow one skilled in the art to envision the structures, sequences or compounds encompassed by the claims. A nucleic acid comprising a fragment of SEQ ID NO: 1 may also comprise a vast variety of other nucleotides, any of which would be expected to have different properties than that of SEQ ID NO: 1....Claims 43-44, 50-53 are directed to nucleic acids encoding polypeptides which are at least 50% identical to recited SEQ ID NO's. The specification discloses that SEQ ID NO: 2 is one polypeptide sequence encoded by SEQ ID NO: 1; however SEQ ID NO: 1 comprises several possible start codons, and may therefore encode several different polypeptides. See below. A polypeptide which does not consist of the entirety of SEQ ID NO: 2 may be encoded by any number and variety of polynucleotide sequences, none of which would necessarily be the same as or similar to SEQ ID NO: 1. The specification does not disclose polypeptide with any degree of identity less than 100% to SEQ ID NO: 2 nor does the specification disclose any polynucleotides encoding a polypeptide with identity to SEQ ID NO: 2 which is less than 100%.

Applicants respectfully traverse the foregoing rejection. However, in an effort to expedite prosecution of the application, and in no way acquiescing to the Examiner's rejection, claims 43 and 44 have been canceled. With respect to the remaining rejected claims, Applicants respectfully submit that there is sufficient written description in Applicants' specification regarding SEQ ID NO:1, and nucleic acid molecules with a significant degree of identity to SEQ ID NO:1 and SEQ ID NO:2, *i.e.*, 90% identity, to inform a skilled artisan that Applicants were in possession of the claimed invention at the time the application was filed as required by section 112, first paragraph (see M.P.E.P. 2163.02). In order to meet the written description requirement of the first paragraph of 35 U.S.C. § 112, it is not necessary that a patent specification describe each and every specific member of a genus recited in a claim.

A claim to a genus of chemical compounds satisfies the written description requirement when its accompanying specification either defines by sequence a representative number of its members falling within the scope of the genus or when its accompanying specification defines the structural features common to a substantial portion of the genus (*The Regents of the University of California v. Eli Lilly and Co.*, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997)). For reasons discussed in detail below, the instant specification satisfies this requirement for the claimed invention.

Example 8 of the *Revised Interim Written Description Guidelines Training Materials* provides that a claim directed to isolated nucleic acid molecules comprising SEQ ID NO:2, which is a DNA fragment encoding a full open reading frame (ORF) satisfies the requirements of 35 U.S.C. §112, first paragraph for written description. The rationale behind the foregoing conclusion, as presented by the *Written Description Guidelines*, is that

[o]ne of skill in the art can readily envisage nucleic acid sequences which include SEQ ID NO:2 because e.g. SEQ ID NO:2 can be readily embedded in known vectors. Although there may be substantial variability among the species of DNAs encompassed within the scope of the claim because SEQ ID NO:2 may be combined with sequences known in the art, e.g., combined with expression vectors, ***the necessary common attribute is the ORF (SEQ ID NO:2).***

Furthermore, the Guidelines state that

weighing all the factors including (1) that the full length ORF (SEQ ID NO:2) is disclosed and (2) that any substantial variability within the genus arises due to addition of elements that are not part of the inventors particular contribution, taken in view of the level of knowledge and skill in the art, ***one skilled in the art would recognize from the disclosure that the applicant was in possession of the genus of DNAs that comprise SEQ ID NO:2.***

Similarly, in the present case, claim 39 is directed to isolated nucleic acid molecules comprising the nucleotide sequence shown in SEQ ID NO:1. As set forth in Example 8 of the *Revised Interim Written Description Guidelines Training Materials*, one of skill in the art can readily envisage nucleic acid sequences which include SEQ ID

NO:1 based on the disclosure of the ORF and the fact that “any substantial variability within the genus arises due to addition of elements that are not part of the inventors particular contribution.” Accordingly, one skilled in the art would recognize that Applicants were in possession of the genus of DNAs that comprise SEQ ID NO:1.

Example 14 of the *Revised Interim Written Description Guidelines Training Materials* provides that a claim directed to variants of a polypeptide having SEQ ID NO:3 “that are at least 95% identical to SEQ ID NO:3 and catalyze the reaction of A→B” with an accompanying specification that discloses a single species falling within the claimed genus, satisfies the requirements of 35 U.S.C. §112, first paragraph for written description. The rationale behind the foregoing conclusion, as presented by the *Written Description Guidelines*, is that “[t]he single species disclosed is representative of the genus because all members have at least 95% structural identity with the reference compound and because of the presence of an assay which Applicant provided for identifying all of the at least 95% identical variants of SEQ ID NO:3 which are capable of the specified catalytic activity.”

Similarly, in the present case, claims 47, 52, and 53 are directed to isolated nucleic acid molecules comprising a nucleotide sequence that is at least 90% identical to the nucleotide sequence shown in SEQ ID NO:1, wherein the nucleotide sequence encodes a polypeptide which is capable of modulating the production of a fine chemical.

Applicants have disclosed in the instant specification assays for identifying all of the at least 90% identical variants of SEQ ID NO:1 which encode polypeptides which are capable of modulating the production of a fine chemical (see, for example, page 16, lines 18-35; page 17 lines 7-21; and page 44, line 6 through page 45, line 14 of the specification). Thus, based on the teachings in Applicants’ specification, one of skill in the art would conclude that Applicants were in possession of the claimed invention at the time of filing.

With respect to claim 49, which is directed to isolated nucleic acid molecules comprising a fragment of at least 30 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:1, or a full complement thereof, Applicants have described various fragments of the polynucleotides of the invention.

In Example 15 of the *Interim Guidelines for Examination of Patent Applications Under the 35 U.S.C. §112, First Paragraph Written Description Requirement* the

“theoretical specification” discloses a messenger RNA sequence, SEQ ID NO:1, which encodes a human growth hormone. The “theoretical specification” claims antisense molecules that inhibit the production of human growth hormone. The Guidelines provide that

[c]onsidering the specification’s disclosure of (1) ***the sequence (SEQ ID NO:1) which defines and limits the structure of any effective molecules such that one skilled in the art would be able to immediately envisage members of the genus embraced by the claim*** and 2) the functional characteristics of the claimed invention as well as a routine art-recognized method of screening for antisense molecules which provide further distinguishing characteristics of the claimed invention, along with, 3) the general level of knowledge and skill in the art, one skilled in the art would conclude that applicant was in possession of the invention.....***the claimed invention is adequately described.***

Similar to Example 15 of the *Interim Guidelines*, the instant specification describes the nucleotide sequence of the nucleic acid molecules of the invention (SEQ ID NO:1) ***which define and limit the structure of any nucleotide fragments such that one skilled in the art would be able to immediately envisage members of the genus embraced by the nucleotide fragment claims.***

Moreover, as provided in Example 15 of the *Interim Guidelines*, the generation of oligonucleotide fragments is routine. For example, (as indicated in Example 15 of the *Interim Guidelines*) any specified fragment can be ordered from a commercial synthesizing service. Finally, Applicants’ specification teaches how such polynucleotide fragments encoding polypeptides may be tested for activity (see, for example, page 21, line 31 through page 22, line 19 and page 38, lines 1-14 of Applicants’ specification).

Based on the foregoing teachings in Applicants’ specification and the knowledge generally available in the art, one skilled in the art would conclude that Applicants were in possession of the claimed invention at the time of filing of the application. The skilled artisan would also be able to make and use the claimed polypeptide fragments using only routine experimentation.

Accordingly, based on the amendments to the claims and the comments set forth above, Applicants respectfully request reconsideration and withdrawal of the instant rejection under 35 U.S.C. § 112, first paragraph.

Rejection of Claims 43, 44, 47, 48, 52, and 53-61 Under 35 U.S.C. 112, First Paragraph

The Examiner has rejected claims 43, 44, 47, 48, 52, and 53-61 under 35 U.S.C. 112, first paragraph, as "containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention." In particular, the Examiner is of the opinion that

[t]he specification discloses in Table 1 that SEQ ID NO: 1 encodes SEQ ID NO: 2, which is a polypeptide. The specification further discloses on pages 21-22 that the inventive nucleic acid molecule encodes an amino acid sequence "sufficiently homologous" to an amino acid sequence of Appendix B such that the protein or portion thereof which is encoded maintains the ability to modulate yield, production, etc. of a fine chemical. None of the sequences shown in Appendix B are identified by SEQ ID NO. However, Table 1 discloses that SEQ ID NO's 1 and 2 are identified as RXN01638, on page 1 of the Table. Appendix B lists a sequence labeled RXN01638, on page 64, which appears to match SEQ ID NO: 2, therefore Appendix B does appear to list the entirety of SEQ ID NO: 2. Appendix B does not appear to list any "portions" or fragments of SEQ ID NO: 2. In addition, Appendix B is merely a listing of amino acid sequences, and contains no information with regard to activity of the peptides represented. Although applicant was clearly in possession of SEQ ID NO: 2 at the time of filing, the specification does not teach anywhere whether SEQ ID NO: 2, or any other peptide encoded by SEQ ID NO: 1 actually has the activity recited in the instant claims. The specification teaches, on pages 51-52, prophetic examples for how to determine the activity, and potential use for production of fine chemicals, of mutant proteins, but does not disclose whether SEQ ID NO:2 is one of the "mutant proteins" to be so tested, nor whether SEQ ID NO: 2 is actually known to have ANY activity, specifically one which modulates the production of fine chemicals. SEQ ID NO: 1 has several potential start codons, and therefore may encode polypeptides or proteins other than SEQ ID NO: 2. If so, these peptides are not disclosed by the instant specification, nor does the instant specification disclose whether any activity is known for peptides other than SEQ ID NO: 2 which may be encoded by SEQ

ID NO: 1. As the instant specification does not teach that SEQ ID NO: 2, or any portion thereof, or any other peptide encoded by SEQ ID NO: 1 was known at the time of filing to have MCP activity and/or activity in modulating the production of fine chemicals, the claims are rejected for lack of written description.

Applicants respectfully traverse the foregoing rejection. However, in an effort to expedite prosecution of the application, and in no way acquiescing to the Examiner's rejection, claims 43 and 44 have been canceled.

With respect to claims 47, 48, 52, and 53-61, the Examiner states that "[a] nucleotide sequence comprising or consisting of SEQ ID NO:1, or a portion thereof, which encodes an MCP polypeptide and/or a polypeptide capable of modulating the production of a fine chemical, are not described by the instant specification." Applicants respectfully submit that, as stated by the Examiner, "the specification discloses in Table 1 that SEQ ID NO:1 encodes SEQ ID NO:2, which is a polypeptide." Table 1 identifies SEQ ID NO:2 as RXN01638. This sequence is set forth in Appendix B at page 136, rather than at page 64 as stated by the Examiner. The same sequence is also disclosed in Applicants' Sequence Listing at pages 2-3, and identified as SEQ ID NO:2. One of ordinary skill in the art would recognize, by reading Table 1 and Applicants' specification, that SEQ ID NO:1 encodes SEQ ID NO:2, which is also identified as RXN01638.

Claims 47 and 48 are directed to isolated nucleic acid molecules comprising or consisting of a nucleotide sequence which is at least 90% identical to the nucleotide sequence of SEQ ID NO:1, or a complement thereof, where the nucleotide sequence encodes a polypeptide which is capable of modulating the production of a fine chemical. Claims 52 and 53 are directed to isolated nucleic acid molecules which encodes a polypeptide comprising or consisting of an amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO:2, where the polypeptide is a MCP polypeptide and where the polypeptide is capable of modulating the production of a fine chemical.

Applicants specification describes an "MCP protein" or an "MCP polypeptide" as a protein or polypeptide which is

able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target

protein for drug screening or design, or to serve as identifying markers for *C. glutamicum* or related organisms. Examples of MCP proteins include those encoded by the MCP genes set forth in Table 1 and Appendix A. (see page 15, lines 8-13 of Applicants' specification).

Applicants respectfully submit that SEQ ID NO:2 is included within this definition as it is a polypeptide encoded by SEQ ID NO:1, as set forth in the Sequence Listing and in Appendix A.

As set forth above, Applicants have disclosed in the instant specification assays for identifying all of the at least 90% identical variants of SEQ ID NO:1 which encode polypeptides which are capable of modulating the production of a fine chemical (see, for example, page 16, lines 18-35; page 17 lines 7-21; and page 44, line 6 through page 45, line 14 of the specification). Thus, based on the teachings in Applicants' specification, one of skill in the art would conclude that Applicants were in possession of the claimed invention at the time of filing. Accordingly, Applicants respectfully request reconsideration and withdrawal of the foregoing rejection.

Rejection of Claims 39-42, 45-49, and 54-61 Under 35 USC § 112, Second Paragraph

The Examiner has rejected claims 39-42, 45-49, and 54-61 under 35 U.S.C. 112, second paragraph, as "being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention." In particular, the Examiner is of the opinion that "[t]he term "complement" is not defined by the specification and may have several meanings in the art; e.g. a sequence which is partially complementary to, a sequence which is fully complementary to, or a sequence with a specified degree or percentage of complementarity to the elected SEQ ID NO: As the metes and bounds intended by applicant for a "complement" are unclear, the claims are indefinite."

Applicants respectfully traverse the foregoing rejection. However, in an effort to expedite prosecution, and in no way acquiescing to the Examiner's rejection, Applicants have amended claims 39-42 and 45-49 to recite the phrase "full complement thereof." Applicants submit that amended claims 39-42 and 45-49, and dependent claims 54-61, are

clear and definite. Accordingly, Applicants respectfully request reconsideration and withdrawal of the foregoing rejection.

Rejection of Claim 49 Under 35 USC § 102

The Examiner has rejected claim 49 under 35 U.S.C. 102(b) as “being anticipated by SAITO et al. (US 5,665,872).” In particular, the Examiner is of the opinion that “SAITO teaches SEQ ID NO's 5 and 6 (col's 39-62), each of which encodes an LDL receptor protein and comprises a fragment of 22 contiguous nucleotides which are 100% identical to residues 165-186 of instant SEQ ID NO: 1, thus anticipating claim 49.”

Applicants respectfully traverse the foregoing rejection. However, in an effort to expedite prosecution, and in no way acquiescing to the Examiner's rejection, Applicants have amended claim 49 such that it is directed to isolated nucleic acid molecules comprising a fragment of at least 30 contiguous nucleotides of SEQ ID NO:1. Accordingly, Applicants respectfully request reconsideration and withdrawal of the foregoing rejection.

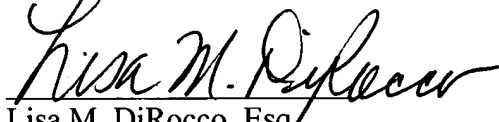
The Examiner has also rejected claim 49 under 35 U.S.C. 102(b) as “being anticipated by MICHAELS et al. (US 5,554,534).” In particular, the Examiner is of the opinion that “MICHAELS teaches SEQ ID NO: 3 (col's 27-30), which comprises a fragment of 20 contiguous nucleotides which is 100% identical to residues 489-508 of instant SEQ ID NO: 1, thus anticipating claim 49.”

Applicants respectfully traverse the foregoing rejection. However, in an effort to expedite prosecution, and in no way acquiescing to the Examiner's rejection, Applicants have amended claim 49 such that it is directed to isolated nucleic acid molecules comprising a fragment of at least 30 contiguous nucleotides of SEQ ID NO:1. Accordingly, Applicants respectfully request reconsideration and withdrawal of the foregoing rejection.

SUMMARY

If a telephone conversation with Applicants' Attorney would expedite the prosecution of the above-identified application, the examiner is urged to call the undersigned at (617) 227-7400.

Respectfully submitted,



Lisa M. DiRocco, Esq.
Registration No. 51,609
Attorney for Applicants

LAHIVE & COCKFIELD, LLP
28 State Street
Boston, MA 02109
Tel. (617) 227-7400

Dated: **February 28, 2003**

VERSION WITH MARKINGS TO SHOW CHANGES MADE**In the Specification:**

The paragraph beginning at page 54, line 33 has been amended as follows:

--The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com> the Accelrys™ website), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.--

In the Claims:

Please cancel claims 43, 44, and 62, without prejudice, and amend claims 39-42 and 45-53 as follows:

39. (Amended) An isolated nucleic acid molecule comprising the nucleotide sequence set forth in SEQ ID NO:1, ~~SEQ ID NO:7, SEQ ID NO:13, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NO:25, SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37, or SEQ ID NO:41~~, or a full complement thereof.

40. (Amended) An isolated nucleic acid molecule consisting of the nucleotide sequence set forth in SEQ ID NO:1, ~~SEQ ID NO:7, SEQ ID NO:13, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NO:25, SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37, or SEQ ID NO:41~~, or a full complement thereof.

41. (Amended) An isolated nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, ~~SEQ ID NO:8, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, or SEQ ID NO:42~~, or a full complement thereof.

42. (Amended) An isolated nucleic acid molecule which encodes a polypeptide consisting of the amino acid sequence set forth in SEQ ID NO:2, ~~SEQ ID NO:8, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, or SEQ ID NO:42,~~ or a full complement thereof.

45. (Amended) An isolated nucleic acid molecule comprising a nucleotide sequence which is at least ~~90~~50% identical to the nucleotide sequence of SEQ ID NO:1, ~~SEQ ID NO:7, SEQ ID NO:13, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NO:25, SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37, or SEQ ID NO:41,~~ or a full complement thereof.

46. (Amended) An isolated nucleic acid molecule consisting of a nucleotide sequence which is at least ~~90~~50% identical to the nucleotide sequence of SEQ ID NO:1, ~~SEQ ID NO:7, SEQ ID NO:13, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NO:25, SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37, or SEQ ID NO:41,~~ or a full complement thereof.

47. (Amended) An isolated nucleic acid molecule comprising a nucleotide sequence which is at least ~~90~~50% identical to the nucleotide sequence of SEQ ID NO:1, ~~SEQ ID NO:7, SEQ ID NO:13, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NO:25, SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37, or SEQ ID NO:41,~~ or a complement thereof, wherein said nucleotide sequence encodes a polypeptide which is capable of modulating the production of a fine chemical.

48. (Amended) An isolated nucleic acid molecule consisting of a nucleotide sequence which is at least ~~90~~50% identical to the nucleotide sequence of SEQ ID NO:1, ~~SEQ ID NO:7, SEQ ID NO:13, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NO:25, SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37, or SEQ ID NO:41,~~ or a full complement thereof, wherein said nucleotide sequence encodes a polypeptide which is capable of modulating the production of a fine chemical.

49. (Amended) An isolated nucleic acid molecule comprising a fragment of at least ~~15~~ 30 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:1, ~~SEQ~~

~~ID NO:7, SEQ ID NO:13, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NO:25, SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37, or SEQ ID NO:41, or a full complement thereof.~~

50. (Amended) An isolated nucleic acid molecule which encodes a polypeptide comprising an amino acid sequence at least 90~~50~~% identical to the amino acid sequence of SEQ ID NO:2, ~~SEQ ID NO:8, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, or SEQ ID NO:42.~~

51. (Amended) An isolated nucleic acid molecule which encodes a polypeptide consisting of an amino acid sequence at least 90~~50~~% identical to the amino acid sequence of SEQ ID NO:2, ~~SEQ ID NO:8, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, or SEQ ID NO:42.~~

52. (Amended) An isolated nucleic acid molecule which encodes a polypeptide comprising an amino acid sequence at least 90~~50~~% identical to the amino acid sequence of SEQ ID NO:2, ~~SEQ ID NO:8, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, or SEQ ID NO:42,~~ wherein said polypeptide is a MCP polypeptide and wherein said polypeptide is capable of modulating the production of a fine chemical.

53. (Amended) An isolated nucleic acid molecule which encodes a polypeptide consisting of an amino acid sequence at least 90~~50~~% identical to the amino acid sequence of SEQ ID NO:2, ~~SEQ ID NO:8, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, or SEQ ID NO:42~~ wherein said polypeptide is a MCP polypeptide and wherein said polypeptide is capable of modulating the production of a fine chemical.

54. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 39-42, and a nucleotide sequence encoding a heterologous polypeptide.

55. A vector comprising the nucleic acid molecule of any one of claims 39-42.

56. The vector of claim 55, which is an expression vector.
-
57. A host cell transfected with the expression vector of claim 56.
58. The host cell of claim 57, wherein said cell is a bacterial cell.
59. The host cell of claim 58, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
60. The host cell of claim 59, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
61. The host cell of claim 60, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.